

SEQUENCE LISTING

<110> LIN, LEU-FEN H

COLLINS, FRANKLIN D

DOHERTY, DANIEL H

LILE, JACK

BEKTESH, SUSAN

<120> Glial Cell Line-Derived Neurotrophic Factor

<130> S-225E Rev

<140> 08/182,183

<141> 1994-05-23

<150> 07/764,685

<151> 1991-09-20

<150> 07/774,109

<151> 1991-10-08

<150> 07/788,423

<151> 1991-11-06

<150> 07/855,413

<151> 1992-03-19

<150> PCT/US92/07888

<151> 1992-09-17

<160> 28

<170> PatentIn version 3.1

<210> 1

<211> 25

<212> PRT

<213> Rattus rattus

<220>

<221> MISC_FEATURE

<222> (16)..(16)

<223> Xaa in position 16 may be any one of the 20 naturally occurring a
mino acids.

<220>

<221> MISC_FEATURE

<223> N-terminal fragment

<400> 1

Ser Pro Asp Lys Gln Ala Ala Ala Leu Pro Arg Arg Glu Arg Asn Xaa
1 5 10 15

Gln Ala Ala Ala Ala Ser Pro Asp Asn
20 25

<210> 2

<211> 13

<212> PRT

<213> Rattus rattus

<220>

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<222> (2)..(2)

<223> Xaa in position 2 is either Lys or Gln

<220>

<221> MISC_FEATURE

<223> Internal GDNF peptide fragment

<400> 2

Asp Xaa Ile Leu Lys Asn Leu Gly Arg Val Arg Arg Leu
1 5 10

<210> 3

<211> 900

<212> DNA

<213> Rattus rattus

<220>

<221> CDS

<222> (25)..(705)

<223>

<220>

<221> mat_peptide

<222> (304)..()

<223>

<400> 3

ccccccgggct gcaggaattc gggg gtc tac gga gac cgg atc cga ggt gcc
 Val Tyr Gly Asp Arg Ile Arg Gly Ala
 -90 -85

51

* gcc gcc gga cgg gac tct aag atg aag tta tgg gat gtc gtg gct gtc
 Ala Ala Gly Arg Asp Ser Lys Met Lys Leu Trp Asp Val Val Ala Val
 -80 -75 -70

99

tgc ctg gtg ttg ctg cac acc gcg tct gcc ttc ccg ctg ccc gcc ggt
 Cys Leu Val Leu Leu His Thr Ala Ser Ala Phe Pro Leu Pro Ala Gly
 -65 -60 -55

147

aag agg ctt ctc gaa gcg ccc gcc gaa gac cac tcc ctc ggc cac cgc
 Lys Arg Leu Leu Glu Ala Pro Ala Glu Asp His Ser Leu Gly His Arg
 -50 -45 -40

195

cgc gtg ccc ttc gcg ctg acc agt gac tcc aat atg ccc gaa gat tat
 Arg Val Pro Phe Ala Leu Thr Ser Asp Ser Asn Met Pro Glu Asp Tyr
 -35 -30 -25

243

cct gac cag ttt gat gac gtc atg gat ttt att caa gcc acc atc aaa
 Pro Asp Gln Phe Asp Asp Val Met Asp Phe Ile Gln Ala Thr Ile Lys
 -20 -15 -10 -5

291

5 4 0 K
 aga ctg aaa agg tca cca gat aaa caa gcg gcg gca ctt cct cga aga
 Arg Leu Lys Arg Ser Pro Asp Lys Gln Ala Ala Leu Pro Arg Arg
 -1 1 5 10

339

gag agg aac cgg caa gct gca gct gcc agc cca gag aat tcc aga ggg
 Glu Arg Asn Arg Gln Ala Ala Ala Ser Pro Glu Asn Ser Arg Gly
 15 20 25

387

aaa ggt cgc aga ggc cag agg ggc aaa aat cgg ggg tgc gtc tta act
 Lys Gly Arg Arg Gly Gln Arg Gly Lys Asn Arg Gly Cys Val Leu Thr
 30 35 40

435

gca ata cac tta aat gtc act gac ttg ggt ttg ggc tac gaa acc aag
 Ala Ile His Leu Asn Val Thr Asp Leu Gly Leu Gly Tyr Glu Thr Lys
 45 50 55 60

483

gag gaa ctg atc ttt cga tat tgt agc ggt tcc tgt gaa ggc gcc gag 531
 Glu Glu Leu Ile Phe Arg Tyr Cys Ser Gly Ser Cys Glu Ala Ala Glu
 65 70 75

aca atg tac gac aaa ata cta aaa aat ctg tct cga agt aga agg cta 579
 Thr Met Tyr Asp Lys Ile Leu Lys Asn Leu Ser Arg Ser Arg Arg Leu
 80 85 90

aca agt gac aag gta ggc cag gca tgt tgc agg ccg gtc gcc ttc gac 627
 Thr Ser Asp Lys Val Gly Gln Ala Cys Cys Arg Pro Val Ala Phe Asp
 95 100 105

gac gac ctg tcg ttt tta gac gac agc ctg gtt tac cat atc cta aga 675
 Asp Asp Leu Ser Phe Leu Asp Asp Ser Leu Val Tyr His Ile Leu Arg
 110 115 120

aag cat tcc gct aaa cgg tgt gga tgt atc tgaccctggc tccagagact 725
 Lys His Ser Ala Lys Arg Cys Gly Cys Ile
 125 130

gctgtgtatt gcattcctgc tacactgcga agaaaaggac caaggttccc aggaaatatt 785

tgcccagaaa ggaagataag gaccaagaag gcagaggcag aggcggaaga agaagaagaa 845

aagaaggacg aaggcagcca tctgtggag cctgtagaag gaggcccagc tacag 900

<210> 4

<211> 227

<212> PRT

<213> Rattus rattus

<400> 4

Val Tyr Gly Asp Arg Ile Arg Gly Ala Ala Ala Gly Arg Asp Ser Lys
 -90 -85 -80

Met Lys Leu Trp Asp Val Val Ala Val Cys Leu Val Leu Leu His Thr
 -75 -70 -65

Ala Ser Ala Phe Pro Leu Pro Ala Gly Lys Arg Leu Leu Glu Ala Pro
 -60 -55 -50

Ala Glu Asp His Ser Leu Gly His Arg Arg Val Pro Phe Ala Leu Thr
 -45 -40 -35 -30

Ser Asp Ser Asn Met Pro Glu Asp Tyr Pro Asp Gln Phe Asp Asp Val
 -25 -20 -15

Met Asp Phe Ile Gln Ala Thr Ile Lys Arg Leu Lys Arg Ser Pro Asp
 -10 -5 -1 1

Lys Gln Ala Ala Ala Leu Pro Arg Arg Glu Arg Asn Arg Gln Ala Ala
 5 10 15

Ala Ala Ser Pro Glu Asn Ser Arg Gly Lys Gly Arg Arg Gly Gln Arg
 20 25 30 35

Gly Lys Asn Arg Gly Cys Val Leu Thr Ala Ile His Leu Asn Val Thr
 40 45 50

Asp Leu Gly Leu Gly Tyr Glu Thr Lys Glu Glu Leu Ile Phe Arg Tyr
 55 60 65

Cys Ser Gly Ser Cys Glu Ala Ala Glu Thr Met Tyr Asp Lys Ile Leu
 70 75 80

Lys Asn Leu Ser Arg Ser Arg Arg Leu Thr Ser Asp Lys Val Gly Gln
 85 90 95

Ala Cys Cys Arg Pro Val Ala Phe Asp Asp Asp Leu Ser Phe Leu Asp
 100 105 110 115

Asp Ser Leu Val Tyr His Ile Leu Arg Lys His Ser Ala Lys Arg Cys
 120 125 130

Gly Cys Ile

<210> 5

<211> 562

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (24)..(506)

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<221> mat_peptide

<222> (105)..()

<223>

<400> 5

attttctttt ttctttttga aca agc aat atg cca gag gat tat cct gat cag
 Ser Asn Met Pro Glu Asp Tyr Pro Asp Gln
 -25 -20

53

ttc gat gat gtc atg gat ttt att caa gcc acc att aaa aga ctg aaa
 Phe Asp Asp Val Met Asp Phe Ile Gln Ala Thr Ile Lys Arg Leu Lys
 -15 -10 -5

101

agg tca cca gat aaa caa atg gca gtg ctt cct aga aga gag cggt aat
 Arg Ser Pro Asp Lys Gln Met Ala Val Leu Pro Arg Arg Glu Arg Asn
 -1 1 5 10 15

149

cgg cag gct gca gct gcc aac cca gag aat tcc aga gga aaa ggt cgg
 Arg Gln Ala Ala Ala Asn Pro Glu Asn Ser Arg Gly Lys Gly Arg
 20 25 30

197

aga ggc cag agg ggc aaa aac cgg ggt tgc tta act gca ata cat Arg Gly Gln Arg Gly Lys Asn Arg Gly Cys Val Leu Thr Ala Ile His 35 40 45	245
tta aat gtc act gac ttg ggt ctg ggc tat gaa acc aag gag gaa ctg Leu Asn Val Thr Asp Leu Gly Leu Gly Tyr Glu Thr Lys Glu Glu Leu 50 55 60	293
att ttt agg tac tgc agc ggc tct tgc gat gca gct gag aca acg tac Ile Phe Arg Tyr Cys Ser Gly Ser Cys Asp Ala Ala Glu Thr Thr Tyr 65 70 75	341
gac aaa ata ttg aaa aac tta tcc aga aat aga agg ctg gtg act gac Asp Lys Ile Leu Lys Asn Leu Ser Arg Asn Arg Arg Leu Val Thr Asp 80 85 90 95	389
aaa gta ggg cag gca tgt tgc aga ccc atc gcc ttt gat gat gac ctg Lys Val Gly Gln Ala Cys Cys Arg Pro Ile Ala Phe Asp Asp Asp Leu 100 105 110	437
tcg ttt tta gat gat aac ctg gtt tac cat att cta aga aag cat tcc Ser Phe Leu Asp Asp Asn Leu Val Tyr His Ile Leu Arg Lys His Ser 115 120 125	485
gct aaa agg tgt gga tgt atc tgactccggc tccagagact gctgtgtatt Ala Lys Arg Cys Gly Cys Ile 130	536
gcattcctgc tacagtgc aa agaaag	562
 <210> 6	
 <211> 161	
 <212> PRT	
 <213> Homo sapiens	
 <400> 6	
Ser Asn Met Pro Glu Asp Tyr Pro Asp Gln Phe Asp Asp Val Met Asp -25 -20 -15	
Phe Ile Gln Ala Thr Ile Lys Arg Leu Lys Arg Ser Pro Asp Lys Gln -10 -5 -1 1 5	
Met Ala Val Leu Pro Arg Arg Glu Arg Asn Arg Gln Ala Ala Ala 10 15 20	
Asn Pro Glu Asn Ser Arg Gly Lys Gly Arg Arg Gly Gln Arg Gly Lys 25 30 35	
Asn Arg Gly Cys Val Leu Thr Ala Ile His Leu Asn Val Thr Asp Leu 40 45 50	
Gly Leu Gly Tyr Glu Thr Lys Glu Leu Ile Phe Arg Tyr Cys Ser 55 60 65	
Gly Ser Cys Asp Ala Ala Glu Thr Thr Tyr Asp Lys Ile Leu Lys Asn 70 75 80 85	
Leu Ser Arg Asn Arg Arg Leu Val Thr Asp Lys Val Gly Gln Ala Cys	

90

95

100

Cys Arg Pro Ile Ala Phe Asp Asp Asp Leu Ser Phe Leu Asp Asp Asn
105 110 115

Leu Val Tyr His Ile Leu Arg Lys His Ser Ala Lys Arg Cys Gly Cys
120 125 130

Ile

<210> 7

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide probe

<220>

<221> misc_feature

<222> (3)...(3)

<223> N at position 3 is inosine

<220>

<221> misc_feature

<222> (15)...(15)

<223> N at position 15 is inosine

<220>

<221> misc_feature

<222> (18)...(18)

<223> N at position 18 is inosine

<400> 7

ccngayaarc argcngcngc

20

<210> 8

<211> 223

<212> DNA

<213> Homo sapiens

<400> 8
ttctctcccc cacctcccgac ctgcccgcgc aggtgccggcc gccggacggg actttaagat 60
gaagtttatgg gatgtcgtgg ctgtctgcct ggtgctgctc cacaccgcgt ccgccttccc 120
gctgcccggcc ggtaagaggc ctcccgaggc gcccggccaa gaccgctccc tcggccggcg 180
ccgcgcgcggcc ttcgcgctga gcagtgactg taagaaccgt tcc 223

<210> 9

<211> 12

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide linker

<400> 9
cccgaaattcg gg 12

<210> 10

<211> 7

<212> PRT

<213> Rattus rattus

<400> 10

Pro Asp Lys Gln Ala Ala Ala
1 5

<210> 11

<211> 33

<212> DNA

<213> Artificial sequence

<220>

<223> Nucleic acid sequence from pBluescript SK-76.1 encoding rat GDNF
N-terminus sequence

<400> 11
gagaggaacc ggcaagctgc wgmwgymwgm ccw 33

<210> 12

<211> 11

<212> PRT

<213> Rattus rattus

<400> 12

Glu Arg Asn Arg Gln Ala Ala Ala Ala Ser Pro
1 5 10

<210> 13

<211> 20

<212> DNA

<213> Artificial sequence

<220>

<223> Oligonucleotide PCR primer DHD-26 to amplify DNA encoding rat GDN
F polypeptide

<220>

<221> misc_feature

<222> (9)..(9)

<223> N at position 9 is inosine

<220>

<221> misc_feature

<222> (12)..(12)

<223> N at position 12 is inosine

<400> 13

arrttyttna rnatytrtc

20

<210> 14

<211> 7

<212> PRT

<213> Rattus rattus

<220>

<221> misc_feature

<223> Internal rat GDNF peptide

<400> 14

Asp Lys Ile Leu Lys Asn Leu
1 5

<210> 15

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer PD1 to amplify rat GDNF probe

<400> 15

gacgggactc taagatg

17

<210> 16

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer DHD23 to amplify rat GDNF probe

<220>

<221> misc_feature

<222> (3)..(3)

<223> N at position 3 is inosine

<220>

<221> misc_feature

<222> (6)..(6)

<223> N at position 3 is inosine

<220>

<221> misc_feature

<222> (18)..(18)

<223> N at position 3 is inosine

<400> 16
gcngcngcyt gytttcnngg

20

<210> 17

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer LF2 to amplify rat GDNF probe

<400> 17

cgagacaatg tacgaca

17

<210> 18

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer PD2 to amplify rat GDNF probe

<400> 18

ctctggagcc agggtca

17

<210> 19

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer PD1 to amplify rat GDNF probe

<400> 19

cccgaaattcg acgggactct aagatg

26

<210> 20

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer LFA to amplify rat GDNF probe

<400> 20

cggtggccag agggagtggt cttc

24

<210> 21

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer PD3 to amplify human cDNA

<400> 21

cgccgatcca ataaggagga aaaaaaatgt caccagataa acaaat

46

<210> 22

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer PD4 to amplify human cDNA

<400> 22

cgcggtagccc agtctctgga gccgga

26

<210> 23

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic adapter fragment for plasmid pCJ1

<400> 23

gatctagaat tgtcatgttt gacagcttat cat

33

<210> 24

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> Polylinker sequence for plasmid pCJX1-1 with EcoRI and PstI overhangs

<400> 24

aattcccggtt taccagatct gagctcacta gtctgca

37

<210> 25

<211> 747

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (32)..(691)

<223>

<220>

<221> mat_peptide

<222> (290)..()

<223>

<400> 25

ttctctcccc cacctcccgcc ctgccccgc a ggt gcc gcc gca cgg gac
Gly Ala Ala Ala Gly Arg Asp
-85 -80

52

ttt aag atg aag tta tgg gat gtc gtg gct gtc tgc ctg gtg ctg ctc
Phe Lys Met Lys Leu Trp Asp Val Val Ala Val Cys Leu Val Leu Leu
-75 -70 -65

100

cac acc gcg tcc gcc ttc ccg ctg ccc gcc ggt aag agg cct ccc gag
His Thr Ala Ser Ala Phe Pro Leu Pro Ala Gly Lys Arg Pro Pro Glu
-60 -55 -50

148

gcg ccc gcc gaa gac cgc tcc ctc ggc cgc cgc gca ccc ttc gcg
Ala Pro Ala Glu Asp Arg Ser Leu Gly Arg Arg Ala Pro Phe Ala
-45 -40 -35

196

ctg agc agt gac tca aat atg cca gag gat tat cct gat cag ttc gat
Leu Ser Ser Asp Ser Asn Met Pro Glu Asp Tyr Pro Asp Gln Phe Asp
-30 -25 -20

244

gat gtc atg gat ttt att caa gcc acc att aaa aga ctg aaa agg tca
Asp Val Met Asp Phe Ile Gln Ala Thr Ile Lys Arg Leu Lys Arg Ser

292

-15	-10	-5	-1 1	
cca gat aaa caa atg gca gtg ctt cct aga aga gag	cgg aat cgg cag			340
Pro Asp Lys Gln Met Ala Val Leu Pro Arg Arg Glu Arg Asn Arg Gln				
5	10	15		
gct gca gct gcc aac cca gag aat tcc aga gga aaa ggt	cgg aga ggc			388
Ala Ala Ala Ala Asn Pro Glu Asn Ser Arg Gly Lys Gly Arg Arg Gly				
20	25	30		
cag agg ggc aaa aac cgg ggt tgt gtc tta act gca ata cat tta aat	Gln Arg Gly Lys Asn Arg Gly Cys Val Leu Thr Ala Ile His Leu Asn			436
35	40	45		
gtc act gac ttg ggt ctg ggc tat gaa acc aag gag gaa ctg att ttt	Val Thr Asp Leu Gly Leu Gly Tyr Glu Thr Lys Glu Glu Leu Ile Phe			484
50	55	60	65	
agg tac tgc agc ggc tct tgc gat gca gct gag aca acg tac gac aaa	Arg Tyr Cys Ser Gly Ser Cys Asp Ala Ala Glu Thr Thr Tyr Asp Lys			532
70	75	80		
ata ttg aaa aac tta tcc aga aat aga agg ctg gtg act gac aaa gta	Ile Leu Lys Asn Leu Ser Arg Asn Arg Arg Leu Val Thr Asp Lys Val			580
85	90	95		
ggg cag gca tgt tgc aga ccc atc gcc ttt gat gat gac ctg tcg ttt	Gly Gln Ala Cys Cys Arg Pro Ile Ala Phe Asp Asp Asp Leu Ser Phe			628
100	105	110		
tta gat gat aac ctg gtt tac cat att cta aga aag cat tcc gct aaa	Leu Asp Asp Asn Leu Val Tyr His Ile Leu Arg Lys His Ser Ala Lys			676
115	120	125		
agg tgt gga tgt atc tgactccggc tccagagact gctgtgtatt gcattcctgc	Arg Cys Gly Cys Ile			731
130				
tacagtgcaa agaaaag				747
<210> 26				
<211> 220				
<212> PRT				
<213> Homo sapiens				
<400> 26				
Gly Ala Ala Ala Gly Arg Asp Phe Lys Met Lys Leu Trp Asp Val Val				
-85	-80	-75		
Ala Val Cys Leu Val Leu Leu His Thr Ala Ser Ala Phe Pro Leu Pro				
-70	-65	-60	-55	
Ala Gly Lys Arg Pro Pro Glu Ala Pro Ala Glu Asp Arg Ser Leu Gly				
-50	-45	-40		
Arg Arg Arg Ala Pro Phe Ala Leu Ser Ser Asp Ser Asn Met Pro Glu				
-35	-30	-25		

Asp Tyr Pro Asp Gln Phe Asp Asp Val Met Asp Phe Ile Gln Ala Thr
 -20 -15 -10

Ile Lys Arg Leu Lys Arg Ser Pro Asp Lys Gln Met Ala Val Leu Pro
 -5 -1 1 5 10

Arg Arg Glu Arg Asn Arg Gln Ala Ala Ala Asn Pro Glu Asn Ser
 15 20 25

Arg Gly Lys Gly Arg Arg Gly Gln Arg Gly Lys Asn Arg Gly Cys Val
 30 35 40

Leu Thr Ala Ile His Leu Asn Val Thr Asp Leu Gly Leu Gly Tyr Glu
 45 50 55

Thr Lys Glu Glu Leu Ile Phe Arg Tyr Cys Ser Gly Ser Cys Asp Ala
 60 65 70

Ala Glu Thr Thr Tyr Asp Lys Ile Leu Lys Asn Leu Ser Arg Asn Arg
 75 80 85 90

Arg Leu Val Thr Asp Lys Val Gly Gln Ala Cys Cys Arg Pro Ile Ala
 95 100 105

Phe Asp Asp Asp Leu Ser Phe Leu Asp Asp Asn Leu Val Tyr His Ile
 110 115 120

Leu Arg Lys His Ser Ala Lys Arg Cys Gly Cys Ile
 125 130

<210> 27

<211> 211

<212> PRT

<213> Rattus rattus

<220>

<221> MISC_FEATURE

<223> Rat pre-pro GDNF

<400> 27

Met Lys Leu Trp Asp Val Val Ala Val Cys Leu Val Leu Leu His Thr
 1 5 10 15

Ala Ser Ala Phe Pro Leu Pro Ala Gly Lys Arg Leu Leu Glu Ala Pro
20 25 30

Ala Glu Asp His Ser Leu Gly His Arg Arg Val Pro Phe Ala Leu Thr
35 40 45

Ser Asp Ser Asn Met Pro Glu Asp Tyr Pro Asp Gln Phe Asp Asp Val
50 55 60

Met Asp Phe Ile Gln Ala Thr Ile Lys Arg Leu Lys Arg Ser Pro Asp
65 70 75 80

Lys Gln Ala Ala Ala Leu Pro Arg Arg Glu Arg Asn Arg Gln Ala Ala
85 90 95
Ala Ala Ser Pro Glu Asn Ser Arg Gly Lys Gly Arg Arg Gly Gln Arg
100 105 110
Gly Lys Asn Arg Gly Cys Val Leu Thr Ala Ile His Leu Asn Val Thr
115 120 125
Asp Leu Gly Leu Gly Tyr Glu Thr Lys Glu Glu Leu Ile Phe Arg Tyr
130 135 140
Cys Ser Gly Ser Cys Glu Ala Ala Glu Thr Met Tyr Asp Lys Ile Leu
145 150 155 160
Lys Asn Leu Ser Arg Ser Arg Arg Leu Thr Ser Asp Lys Val Gly Gln
165 170 175
Ala Cys Cys Arg Pro Val Ala Phe Asp Asp Asp Leu Ser Phe Leu Asp
180 185 190
Asp Ser Leu Val Tyr His Ile Leu Arg Lys His Ser Ala Lys Arg Cys
195 200 205
Gly Cys Ile
210

<210> 28

<211> 211

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<223> Human pre-pro GDNF

<400> 28

Met Lys Leu Trp Asp Val Val Ala Val Cys Leu Val Leu Leu His Thr
1 5 10 15
Ala Ser Ala Phe Pro Leu Pro Ala Gly Lys Arg Pro Pro Glu Ala Pro
20 25 30
Ala Glu Asp Arg Ser Leu Gly Arg Arg Arg Ala Pro Phe Ala Leu Ser
35 40 45
Ser Asp Ser Asn Met Pro Glu Asp Tyr Pro Asp Gln Phe Asp Asp Val
50 55 60
Met Asp Phe Ile Gln Ala Thr Ile Lys Arg Leu Lys Arg Ser Pro Asp
65 70 75 80
Lys Gln Met Ala Val Leu Pro Arg Arg Glu Arg Asn Arg Gln Ala Ala
85 90 95

Ala Ala Asn Pro Glu Asn Ser Arg Gly Lys Gly Arg Arg Gly Gln Arg
100 105 110

Gly Lys Asn Arg Gly Cys Val Leu Thr Ala Ile His Leu Asn Val Thr
115 120 125

Asp Leu Gly Leu Gly Tyr Glu Thr Lys Glu Glu Leu Ile Phe Arg Tyr
130 135 140

Cys Ser Gly Ser Cys Asp Ala Ala Glu Thr Thr Tyr Asp Lys Ile Leu
145 150 155 160

Lys Asn Leu Ser Arg Asn Arg Arg Leu Val Thr Asp Lys Val Gly Gln
165 170 175

Ala Cys Cys Arg Pro Ile Ala Phe Asp Asp Asp Leu Ser Phe Leu Asp
180 185 190

Asp Asn Leu Val Tyr His Ile Leu Arg Lys His Ser Ala Lys Arg Cys
195 200 205

Gly Cys Ile
210